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The present invention relates to chemically modified mutant enzymes and a method of producing them and a method of screening them for amidase and/or esterase activity.

Modifying enzyme properties by site-directed mutagenesis has been
20 limited to natural amino acid replacements, although molecular biological strategies for
overcoming this restriction have recently been derived (Cornish et al., Angew. Chem., Int.
Ed. Engl., 34:621-633 (1995)). However, the latter procedures are difficult to apply in
most laboratories. In contrast, controlled chemical modification of enzymes offers broad
potential for facile and flexible modification of enzyme structure, thereby opening up
25 extensive possibilities for controlled tailoring of enzyme specificity.

Changing enzyme properties by chemical modification has been explored previously, with the first report being in 1966 by the groups of Bender (Polgar et al., J. Am. Chem. Soc., 88:3153-3514 (1966)) and Koshland (Neet et al., Proc. Natl. Acad. Sci. USA, 56:1606-1611 (1966)), who created a thiolsubtilisin by chemical transformation (CH₂OH → CH₂SH) of the active site serine residue of subtilisin BPN' to cysteine. Interest in chemically produced artificial enzymes, including some with synthetic potential, was renewed by Wu (Wu et al., J. Am. Chem. Soc., 111:4514-4515 (1989); Bell et al., Biochemistry, 32:3754-3762 (1993)) and Peterson (Peterson et al., Biochemistry,

34:6616-6620 (1995)), and, more recently, Suckling (Suckling et al., Bioorg. Med. Chem. Lett., 3:531-534 (1993)).

- Enzymes are now widely accepted as useful catalysts in organic synthesis. However, natural, wild-type, enzymes can never hope to accept all structures of synthetic chemical interest, nor always be transformed stereospecifically into the desired enantiomerically pure materials needed for synthesis. This potential limitation on the synthetic applicabilities of enzymes has been recognized, and some progress has been made in altering their specificities in a controlled manner using the site-directed and random mutagenesis techniques of protein engineering. However, modifying enzyme properties by protein engineering is limited to making natural amino acid replacements, and molecular biological methods devised to overcome this restriction are not readily amenable to routine application or large scale synthesis. The generation of new specificities or activities obtained by chemical modification of enzymes has intrigued chemists for many years and continues to do so.
- 15 U.S. Patent No. 5,208,158 to Bech et al. ("Bech") describes chemically modified detergent enzymes wherein one or more methionines have been mutated into cysteines. The cysteines are subsequently modified in order to confer upon the enzyme improved stability towards oxidative agents. The claimed chemical modification is the replacement of the thiol hydrogen with C_{1-6} alkyl.
- 20 Although Bech has described altering the oxidative stability of an enzyme through mutagenesis and chemical modification, it would also be desirable to identify one or more enzymes with altered properties such as activity, nucleophile specificity, substrate specificity, stereoselectivity, thermal stability, pH activity profile, and surface binding properties for use in, for example, detergents or organic synthesis. In particular,
- 25 enzymes, such as subtilisins, tailored for peptide synthesis would be desirable. Enzymes useful for peptide synthesis have high esterase and low amidase activities. Generally, subtilisins do not meet these requirements and the improvement of the esterase to amidase selectivities of subtilisins would be desirable as would a rapid identification of subtilisins with improved esterase to amidase selectivities. However, previous attempts to tailor
- 30 enzymes for peptide synthesis by lowering amidase activity have generally resulted in dramatic decreases in both esterase and amidase activities. Previous strategies for lowering the amidase activity include the use of water-miscible organic solvents (Barbas et al., J. Am. Chem. Soc., 110:5162-5166 (1988); Wong et al., J. Am. Chem. Soc.,

- 112:945-953 (1990); and Sears et al., Biotechnol. Prog., 12:423-433 (1996)) and site-directed mutagenesis (Abrahamsen et al., Biochemistry, 30:4151-4159 (1991); Bonneau et al., J. Am. Chem. Soc., 113:1026-1030 (1991); and Graycar et al., Ann. N. Y. Acad. Sci., 67:71-79 (1992)). However, while the ratios of esterase-to-amidase activities were
- 5 improved by these approaches, the absolute esterase activities were lowered concomitantly. Abrahamsen et al., Biochemistry, 30:4151-4159 (1991). Chemical modification techniques (Neet et al., Proc. Nat. Acad. Sci., 56:1606 (1966); Polgar et al., J. Am. Chem. Soc., 88:3153-3154 (1966); Wu et al., J. Am. Chem. Soc., 111:4514-4515 (1989); and West et al., J. Am. Chem. Soc., 112:5313-5320 (1990)), which permit the
- 10 incorporation of unnatural amino acid moieties, have also been applied to improve esterase to amidase selectivity of subtilisins. For example, chemical conversion of the catalytic triad serine (Ser221) of subtilisin to cysteine (Neet et al., Proc. Nat. Acad. Sci., 56:1606 (1966); Polgar et al., J. Am. Chem. Soc., 88:3153-3154 (1966); and Nakatsuka et al., J. Am. Chem. Soc., 109:3808-3810 (1987)) or to selenocysteine (Wu et al., J. Am.
- 15 Chem. Soc., 111:4514-4515 (1989)), and methylation of the catalytic triad histidine (His57) of chymotrypsin (West et al., J. Am. Chem. Soc., 112:5313-5320 (1990)) effected substantial improvement in esterase-to-amidase selectivities. Unfortunately however, these modifications were again accompanied by 50- to 1000-fold decreases in absolute esterase activity.
- 20 Further, previous attempts to identify enzymes with improved esterase to amidase selectivities have resulted in a slow process which requires large quantities of chemically modified mutant enzymes. In particular, the kinetic constants of fully characterized chemically modified mutant enzymes have been evaluated by the method of initial rates with a colorimetric assay. Amidase activity was followed by the release of p-
- 25 nitroanilide from the tetrapeptide substrate succinylalanylalanylpropylphenylalanyl p-nitroanilide (sucAAPF-pNa). The analogous thiobenzyl ester substrate succinyl-alanine-alanine-proline-phenylalanine-thiobenzyl ester (sucAAPF-SBn) does not have a chromogenic leaving group, so detection of hydrolysis requires reaction of the thiobenzyl leaving group with 5,5'-dithiobis-2,2'-nitrobenzoate (DTNB, Ellman's reagent).
- 30 However, the full characterization and kinetic evaluation of new chemically modified mutant enzymes by this method is very material and time-consuming.

The present invention is directed to overcoming these deficiencies.

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SUMMARY OF THE INVENTION

- 5 The present invention relates to a method for screening chemically modified mutant enzymes for amidase and/or esterase activity. This method includes providing a chemically modified mutant enzyme with one or more amino acid residues from an enzyme being replaced by cysteine residues, where at least some of the cysteine residues are modified by replacing thiol hydrogen in the cysteine residues with a thiol side chain, contacting the chemically modified mutant enzyme with a substrate for an amidase and/or a substrate for an esterase, and determining whether the chemically modified mutant enzyme exhibits amidase and/or esterase activity.

- 10 Another aspect of the present invention relates to a chemically modified mutant enzyme with one or more amino acid residues from an enzyme being replaced by cysteine residues, where at least some of the cysteine residues are modified by replacing thiol hydrogen in the cysteine residue with a thiol side chain. The thiol side chain can be $-\text{SCH}_2(p\text{-CH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-OCH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-CF}_3\text{-C}_6\text{H}_4)$, or $-\text{SCH}_2(2,4\text{-diNO}_2\text{-C}_6\text{H}_3)$.

- 15 The present invention also relates to a method of producing a chemically modified mutant enzyme. This method includes providing an enzyme wherein one or more amino acids have been replaced with cysteine residues and replacing thiol hydrogen in at least some of the cysteine residues with a thiol side chain to form the chemically modified mutant enzyme. The thiol side chain can be $-\text{SCH}_2(p\text{-CH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-OCH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-CF}_3\text{-C}_6\text{H}_4)$, or $-\text{SCH}_2(2,4\text{-diNO}_2\text{-C}_6\text{H}_3)$.

- 20 The method for screening chemically modified mutant enzymes for amidase and/or esterase activity of the present invention provides a rapid enzyme modification screen to explore new chemically modified mutant enzymes ("CMMs") without the need to prepare large quantities of the new CMMs and without the material and time-consuming nature of the full characterization and kinetic evaluation of new CMMs.

- 25 The chemically modified mutant enzymes of the present invention exhibit an increased esterase to amidase ratio as compared to wild-type enzymes and, therefore, more efficiently catalyze peptide synthesis. In addition, the

chemically modified mutant enzymes of the present invention are useful in formulating various detergent compositions and in the preparation of animal feed.

BRIEF DESCRIPTION OF THE DRAWINGS

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Figure 1 shows the chemical modification of cysteine mutants of subtilisin *Bacillus lentus* ("SBL") to generate chemically modified mutant enzymes.

Figure 2 shows a 96-well colorimetric assay in accordance with the present invention.

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Figure 3 is a three-dimensional plot of $[k_{cat}/K_M \text{ esterase}]/[k_{cat}/K_M \text{ amidase}]$ v. a-g thiol side chain v. chemically modified mutant, showing the results obtained for the ratio of k_{cat}/K_M for esterase/amidase activity. The reagents are set forth in Figure 1.

Figure 4 shows a comparison of the esterase/amidase specificity ratio from the rapid combinatorial assay of the present invention and the corresponding fully
15 characterized enzymes.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a method for screening chemically
20 modified mutant enzymes for amidase and/or esterase activity. This method includes providing a chemically modified mutant enzyme with one or more amino acid residues from an enzyme being replaced by cysteine residues, where at least some of the cysteine residues are modified by replacing thiol hydrogen in the cysteine residues with a thiol side chain, contacting the chemically modified
25 mutant enzyme with a substrate for an amidase and/or a substrate for an esterase, and determining whether the chemically modified mutant enzyme exhibits amidase and/or esterase activity.

Preferably, the enzyme is a protease. More preferably, the enzyme is a *Bacillus subtilisin*. Subtilisins are alkaline serine proteases that are finding increasing use
30 in biocatalysis, particularly in chiral resolution, regioselective acylation of polyfunctional compounds, peptide coupling, and glycopeptide synthesis. The latter two applications are of particular interest, because they provide an alternative to site-directed mutagenesis and chemical modification for introducing unnatural amino acids into proteins. Subtilisins

- can catalyze peptide bond formation starting from an ester substrate, by first forming an acyl enzyme intermediate which then reacts with a primary amine to form the peptide product. This application thus requires high esterase activity to promote acyl enzyme formation and then low amidase activity to minimize hydrolysis of the peptide bond of the desired product. Generally, subtilisins do not meet these requirements and the identification of subtilisins with improved esterase to amidase selectivities is needed.

- Also, preferably, the amino acids replaced in the enzyme by cysteines are selected from the group consisting of asparagine, leucine, or serine. More preferably, the amino acid to be replaced is located in a subsite of the enzyme, preferably, the S₁, S₁', or S₂ subsites. Most preferably, the amino acids to be replaced are N62, L217, and S166 where the numbered position corresponds to naturally-occurring subtilisin from *Bacillus amyloliquefaciens* or to equivalent amino acid residues in other subtilisins, such as *Bacillus lentus* subtilisin.

- In a particularly preferred embodiment, the enzyme is a *Bacillus lentus* subtilisin. In another particularly preferred embodiment, the amino acid to be replaced by cysteine is N62, L217, or S166 and the thiol side chain group is selected from the group consisting of:

- SCH₂C₆H₅;
- SCH₂(*p*-CH₃-C₆H₄);
- SCH₂(*p*-OCH₃-C₆H₄);
- SCH₂(*p*-COOH-C₆H₄);
- SCH₂C₆F₅;
- SCH₂(*p*-CF₃-C₆H₄); and
- SCH₂(2,4-diNO₂-C₆H₃).

- Preferably, for esterase activity, the ratio of chemically modified mutant enzyme to substrate is from about 1 M:10 M to about 1 M:10⁸ M. Most preferably, the ratio of chemically modified mutant enzyme to substrate is about 1 M:10³ M.

- Preferably, for amidase activity, the ratio of chemically modified mutant enzyme to substrate is from about 1 M:10 M to about 1 M:10¹⁰ M. Most preferably, the ratio of chemically modified mutant enzyme to substrate is about 1 M:6 × 10³ M.

A "chemically modified mutant enzyme" is an enzyme that has been changed by replacing an amino acid residue such as asparagine, leucine, or serine with a cysteine residue and then replacing the thiol hydrogen of the cysteine with a thiol side

chain (e.g., $-\text{SCH}_2\text{C}_6\text{H}_5$, $-\text{SCH}_2(p\text{-CH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-OCH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-COOH-C}_6\text{H}_4)$, $-\text{SCH}_2\text{C}_6\text{F}_5$, $-\text{SCH}_2(p\text{-CF}_3\text{-C}_6\text{H}_4)$, and $-\text{SCH}_2(2,4\text{-diNO}_2\text{-C}_6\text{H}_3)$). After modification, the properties of the enzyme, i.e., activity or substrate specificity, may be altered. Preferably, the activity of the enzyme is increased.

- 5 The term "enzyme" includes proteins that are capable of catalyzing chemical changes in other substances without being changed themselves. The enzymes can be wild-type enzymes or variant enzymes. Enzymes within the scope of the present invention include pullulanases, proteases, cellulases, amylases, isomerases, lipases, oxidases, and reductases. The enzyme can be a wild-type or mutant protease. Wild-type
- 10 proteases can be isolated from, for example, *Bacillus lentus* or *Bacillus amyloliquefaciens* (also referred to as BPN'). Mutant proteases can be made according to the teachings of, for example, PCT Publication Nos. WO 95/10615 and WO 91/06637, which are hereby incorporated by reference.

- Several types of moieties can be used to replace the thiol hydrogen of the
- 15 cysteine residue. These include $-\text{SCH}_2\text{C}_6\text{H}_5$, $-\text{SCH}_2(p\text{-CH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-OCH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-COOH-C}_6\text{H}_4)$, $-\text{SCH}_2\text{C}_6\text{F}_5$, $-\text{SCH}_2(p\text{-CF}_3\text{-C}_6\text{H}_4)$, and $-\text{SCH}_2(2,4\text{-diNO}_2\text{-C}_6\text{H}_3)$.

- The terms "thiol side chain group," "thiol containing group," and "thiol side chain" are terms which are used interchangeably and include groups that are used to
- 20 replace the thiol hydrogen of a cysteine used to replace one of the amino acids in an enzyme. Commonly, the thiol side chain group includes a sulfur through which the thiol side chain groups defined above are attached to the thiol sulfur of the cysteine.

- The binding site of an enzyme consists of a series of subsites across the surface of the enzyme. The substrate residues that correspond to the subsites are labeled
- 25 P and the subsites are labeled S. By convention, the subsites are labeled S_1 , S_2 , S_3 , S_4 , S_1' and S_2' . A discussion of subsites can be found in Siezen et al., Protein Engineering, 4:719-737 (1991) and Fersht, Enzyme Structure and Mechanism, 2 ed., Freeman: New York, 29-30 (1985), which are hereby incorporated by reference. The preferred subsites are S_1 , S_1' and S_2 .

- 30 Another aspect of the present invention relates to chemically modified mutant enzymes with one or more amino acid residues from an enzyme being replaced by cysteine residues, where at least some of the cysteine residues are modified by replacing

thiol hydrogen in the cysteine residue with a thiol side chain to form a chemically modified mutant enzyme. The thiol side chain can be $-\text{SCH}_2(p\text{-CH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-OCH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-CF}_3\text{-C}_6\text{H}_4)$, or $-\text{SCH}_2(2,4\text{-diNO}_2\text{-C}_6\text{H}_3)$.

- 5 The present invention also relates to a method of producing a chemically modified mutant enzyme. This method involves providing an enzyme wherein one or more amino acids have been replaced with cysteine residues and replacing thiol hydrogen in at least some of the cysteine residues with a thiol side chain to form the chemically modified mutant enzyme. The thiol side chain can be $-\text{SCH}_2(p\text{-CH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-OCH}_3\text{-C}_6\text{H}_4)$, $-\text{SCH}_2(p\text{-CF}_3\text{-C}_6\text{H}_4)$, or $-\text{SCH}_2(2,4\text{-diNO}_2\text{-C}_6\text{H}_3)$.

- 10 The amino acid residues of the present invention can be replaced with cysteine residues using site-directed mutagenesis methods or other methods well known in the art. See, for example, PCT Publication No. WO 95/10615, which is hereby incorporated by reference. One method of modifying the thiol hydrogen of the cysteine residue is set forth in the Examples.

- 15 The modified enzymes of the present invention can be formulated into known powdered and liquid detergents having a pH between 6.5 and 12.0 at levels of about 0.01 to about 5% (preferably 0.1% to 0.5%) by weight. These detergent cleaning compositions or additives can also include other enzymes, such as known proteases, amylases, cellulases, lipases, or endoglycosidases, as well as builders and stabilizers.

- 20 The modified enzymes of the present invention, especially subtilisins, are useful in formulating various detergent compositions. A number of known compounds are suitable surfactants useful in compositions comprising the modified enzymes of the present invention. These include nonionic, anionic, cationic, anionic, or zwitterionic detergents, as disclosed in U.S. Patent No. 4,404,128 to Anderson and U.S. Patent No. 4,261,868 to Flora et al., which are hereby incorporated by reference. A suitable
25 detergent formulation is that described in Example 7 of U.S. Patent No. 5,204,015 to Caldwell et al., which is hereby incorporated by reference. The art is familiar with the different formulations which can be used as cleaning compositions. In addition to typical cleaning compositions, it is readily understood that the modified enzymes of the present
30 invention may be used for any purpose that native or wild-type enzymes are used. Thus, these modified enzymes can be used, for example, in bar or liquid soap applications, dishcare formulations, contact lens cleaning solutions or products, peptide synthesis, feed applications such as feed additives or preparation of feed additives, waste treatment,

textile applications such as the treatment of fabrics, and as fusion-cleavage enzymes in protein production. The modified enzymes of the present invention may comprise improved wash performance in a detergent composition (as compared to the precursor).

As used herein, improved wash performance in a detergent is defined as increasing

- 5 cleaning of certain enzyme-sensitive stains such as grass or blood, as determined by light reflectance evaluation after a standard wash cycle.

The addition of the modified enzymes of the present invention to conventional cleaning compositions does not create any special use limitation. In other words, any temperature and pH suitable for the detergent is also suitable for the present
10 compositions as long as the pH is within the above range and the temperature is below the described modified enzyme's denaturing temperature. In addition, modified enzymes in accordance with the invention can be used in a cleaning composition without detergents, again either alone or in combination with builders and stabilizers.

In another aspect of the present invention, the modified enzymes are used
15 in the preparation of an animal feed, for example, a cereal-based feed. The cereal can be at least one of wheat, barley, maize, sorghum, rye, oats, triticale, and rice. Although the cereal component of a cereal-based feed constitutes a source of protein, it is usually necessary to include sources of supplementary protein in the feed such as those derived from fish-meal, meat-meal, or vegetables. Sources of vegetable proteins include at least
20 one of full fat soybeans, rapeseeds, canola, soybean-meal, rapeseed-meal, and canola-meal.

The inclusion of a modified enzyme of the present invention in an animal feed can enable the crude protein value and/or digestibility and/or amino acid content and/or digestibility coefficients of the feed to be increased. This permits a reduction in
25 the amounts of alternative protein sources and/or amino acids supplements which had previously been necessary ingredients of animal feeds.

The feed provided by the present invention may also include other enzyme supplements such as one or more of β -glucanase, glucoamylase, mannanase, α -galactosidase, phytase, lipase, α -arabinofuranosidase, xylanase, α -amylase, esterase,
30 oxidase, oxido-reductase, and pectinase. It is particularly preferred to include a xylanase as a further enzyme supplement such as a subtilisin derived from the genus *Bacillus*. Such xylanases are, for example, described in detail in PCT Patent Application No. WO 97/20920, which is hereby incorporated by reference.

Another aspect of the present invention is a method of treating a textile. This method involves providing a chemically modified mutant enzyme with one or more amino acid residues from an enzyme being replaced by cysteine residues, where at least some of the cysteine residues are modified by replacing thiol hydrogen in the cysteine residues with a thiol side chain. The chemically modified mutant enzyme is contacted with a textile under conditions effective to produce a textile resistant to certain enzyme-sensitive stains. Such enzyme sensitive stains include grass or blood. Preferably, the textile includes a modified enzyme. The method can be used to treat, for example, silk or wool as described in publications such as Research Disclosure 216,034, European Patent Application No. 134,267, U.S. Patent No. 4,533,359, and European Patent Application No. 344,259, which are hereby incorporated by reference.

EXAMPLES

15 **Example 1 – Validation of Rapid Combinatorial Assay for the Preparation and Screening of Chemically Modified Mutant Enzymes for Amidase and Esterase Activities**

20 In a 96-well enzyme activity assay, k_{cat}/K_M is obtained from the rate of product formation (v), using the limiting case of the Michaelis-Menten equation at low substrate concentration as an approximation (Equation 1, where $[S]$ and $[E]$ are the substrate and enzyme concentrations, respectively):

$$V \approx (k_{cat}/K_M) [S][E] \text{ for } [S] \ll K_M$$

(Equation 1)

25 Enzyme stock solutions were prepared in 5 mM 4-morpholineethanesulfonic acid ("MES") with 2 mM CaCl_2 , pH 6.5 at about $5 \times 10^{-7}\text{M}$ for amidase and $5 \times 10^{-9}\text{M}$ for esterase assays. Substrate solutions were prepared in dimethyl sulfoxide ("DMSO"). The amidase substrate sucAAPF-pNa stock was 1.6 mM, which gave 0.08 mM in the well. The esterase substrate succinyl-alanine-alanine-proline-phenylalanine-thiobenzyl ester ("sucAAPF-SBn") stock solution was 1.0 mM, which
30 gave 0.05 mM in the well. Assays were carried out in 0.1M tris hydroxymethylaminomethane ("Tris") pH 8.6 with 0.005% Tween. Tris buffer for the esterase assay contained 0.375 nM DTNB. This buffer had to be used immediately, as the DTNB decomposed within a few hours due to the high pH of the buffer. Berglund et al.,

Bioorg. Med. Chem. Lett., 6:2507-2512 (1996) and Berglund et al., J. Am. Chem. Soc., 119:5265-5266 (1997), which are hereby incorporated by reference.

- A sample of each enzyme solution (~150 μL) was placed in a well in the 1st, 5th, or 9th column of an enzyme loading plate. Rows A to G contained enzymes, and row H contained MES buffer. On a separate assay plate (Corning, flat bottom, 96-well), 10 μL of substrate solution and 180 μL of buffer were dispensed into wells along columns to be used in a run. Columns 1-4 on the assay plate contained four replicates of the enzymes in column 1 of the loading plate; columns 5-8 contained four replicates of the enzymes in column 5 of the loading plate; and columns 9-12 contained four replicates of the enzymes in column 9 of the loading plate. Reactions were initiated by transferring 10 μL of enzyme solution from the loading plate to the assay plate with an 8-channel pipette. For amidase assays, four columns were initiated for one run. For esterase assays, two columns were initiated for one run. The time delay between addition of enzyme to the first column and onset of reading was 22-30 seconds (amidase) and 10-15 seconds (esterase). Immediately after initiation, the plate was placed on a Titertech Multiscan MCC340 reader (programmed in the kinetic mode, filter 414 nm, lag time 0.0 minutes, interval 5 seconds, with automatic background subtraction of blank row H) (Labsystems, Finland) and was read for 1.0 minute (amidase) or 30 seconds (esterase). Prolonged reading, past the nearly linear part of the progress curve (up to ~50% conversion), provided an underestimate of the rate. The output from the reader represented the average rate of change in absorbance at 414 nm min^{-1} , measured at 5 second intervals, of the total time programmed. These data were converted to rates in Ms^{-1} using $\epsilon_{414}=8581 \text{ M}^{-1}\text{cm}^{-1}$ for p-nitroanilide $\epsilon_{414} = 8708 \text{ M}^{-1}\text{cm}^{-1}$ for 3-carboxylate-4-nitrothiophenolate. Both extinction coefficients were determined on the reader using the same conditions and background subtraction as in the assay. The path length was 5 mm. The rates were corrected for active enzyme concentration, and the four replicates for each enzyme were averaged.

Table 1. k_{cat}/K_M obtained for amidase activity at pH 8.6^a

Enzyme	Type of Assay	k_{cat}/K_M (s ⁻¹ mM ⁻¹)
WT	cuvette ^b (standard ^c)	76 ± 7^f
WT	Cuvette (low substrate ^d)	75
WT	96-well ^e (low substrate)	75 ± 5^f
WT	96-well (standard)	80 ± 17^c
L217C- SCH ₂ C ₆ H ₅	96-well (low substrate)	52 ± 6^f
L217C-S CH ₂ C ₆ H ₅	96-well (standard)	48 ± 3^c
L217C- S(CH ₂) ₅ CH ₃	96-well (low substrate)	113 ± 18^f
L217C- S(CH ₂) ₅ CH ₃	96-well (standard)	97 ± 12^c

^a All assays were done at room temperature (ca. 20°C). For assays in 1 mL cuvettes, the cell holder was thermostatted to 20°C.

^b Kinetic assay in 1 mL cuvettes.

^c Complete enzyme kinetics by the method of initial rates, where k_{cat}/K_M was obtained from k_{cat} and K_M values and the errors were obtained from the curve-fitting error in k_{cat} and K_M .

^d Measurement of k_{cat} and K_M using the low substrate approximation (see text).

^e Assay performed on microtiter plates instead of cuvettes.

^f Mean \pm standard error of 4 replicates.

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The value of k_{cat}/K_M (amidase) obtained using the 96-well assay (Table 1) was the same as value obtained by the method of initial rates in 1mL cuvettes at room temperature. The k_{cat}/K_M (amidase) values obtained for WT and CMMs at 25°C were 2 times higher than the values obtained at room temperature.

15 Normally, the cuvette assay is performed at 25°C. The k_{cat}/K_M value obtained in the cuvette at 20°C using a complete kinetic evaluation and the value calculated from the rate at the lowest substrate concentration (Equation 1) were the same, indicating that the low substrate approximation held for WT (Table 1).

To further validate the method, complete kinetic experiments were
20 performed on 96-well plates by running 8 different substrate concentrations along

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the rows and one enzyme/column. Values of k_{cat}/K_M obtained from these experiments were the same as values obtained with the low substrate approximation for WT and two L217C CMMs, indicating that the low substrate approximation also held for CMMs. Similarly, k_{cat}/K_M values for esterase obtained on the plate did not differ significantly from values obtained with the standard assay (Table 2).

Table 2. k_{cat}/K_M obtained for esterase activity at pH 8.6^a

Enzyme	Type of Assay	k_{cat}/K_M ($s^{-1}mM^{-1}$)
WT	96-well (low substrate)	3321 ± 256
L217C	Cuvette (standard)	5540 ± 798
L217C	96-well (low substrate)	5563 ± 419
N62C	Cuvette (standard)	4380 ± 655
N62C	96-well (low substrate)	4151 ± 198
N62C-SCH ₃	Cuvette (standard)	10100 ± 1287
N62C-SCH ₃	96-well (low substrate)	8739 ± 765

^a Notation as in Table 1.

In the esterase assay, temperature did not have a significant effect.

Example 2 – Generation of an Array of New CMMs on a 96-well plate and Screening of the New CMMs for Amidase and Esterase Activity Using the Rapid Combinatorial Assay for the Preparation and Screening of Chemically Modified Mutant Enzymes for Amidase and Esterase Activities

For the small-scale preparation of new CMMs, combinations of 7 different aromatic methanethiosulfonate (“MTS”) reagents (1 a-g) (Figure 1) and 3 cysteine mutants (N62C, L217C and S166C), as well as a WT control were set up on a 96-well plate as shown in the top part of Figure 2. Two replicates of each mutant were prepared with each reagent. One reagent, benzyl MTS (1a), had already been evaluated in large scale modifications, and was included for comparative purposes. The reaction mixture in each well consisted of 20 μ L of enzyme solution (in 5mM MES, 2 mM CaCl₂, pH 6.5, ca, 8×10^5 M), 40 μ L of 2-

[N-cyclohexylamino]ethanesulfonic acid ("CHES") buffer (70 mM CHES, 5mM MES, 2mM CaCl₂, pH 9.5) and 10 μ L of MTS reagent in acetonitrile (ca. 1×10^2 M). The blanks on the reaction plate were 20 μ L of MES, 40 μ L of CHES and 10 μ L of acetonitrile.

- 5 The reactions were left at room temperature and were tested for free thiol groups after 2 hours as follows. On a separate plate, 10 μ L of reaction mixture was added to 60 μ L of DTNB-containing Tris buffer (pH 8.6) and the monitoring plate was scanned at 414 nm 15 minutes later. No difference between the WT and the modified cysteine mutants were detected, indicating that the
- 10 reaction was complete. To quench the reaction, 10 μ L of MES, at a pH of 6.5 was added to each well, and 20 μ L of the mixture from each well was diluted with 980 μ L of MES buffer (in Eppendorf tubes). An amidase loading plate was prepared with the diluted mixtures; an esterase loading plate was prepared with 10 μ L of diluted mixture and 90 μ L of MES buffer in the appropriate wells. From this
- 15 point on, the assays were the same as described in Example 1. Each reaction replicate was assayed in duplicate. The k_{cat}/K_M values were calculated according to Equation 1, basing $[E]$ on the concentration of active enzyme in the parent mutant and assuming no significant denaturation. Since little difference was observed between the two reaction replicates, the 4 values for each combination
- 20 were averaged in the final results.

The amidase k_{cat}/K_M value for N62C-a and S166C-a obtained in the screen was about 2 times lower than the value obtained for the fully characterized enzymes (Table 3), consistent with the previous assay validation results in Example 1.

Table 3. Comparison of data from the screen and the corresponding fully characterized enzymes.

Enzyme	Reagent	Amidase k_{cat}/K_M ($s^{-1} mM^{-1}$) ^a	Amidase k_{cat}/K_M ($s^{-1} Mm^{-1}$) ^b	Esterase k_{cat}/K_M ($s^{-1} mM^{-1}$) ¹	Amidase k_{cat}/K_M ($s^{-1} mM^{-1}$) ²
		Screen	Fully characterized	Screen	Fully characterized
WT		121 ± 3	178 ± 15	3890 ± 170	3560 ± 540
N62C	1a	207 ± 13	379 ± 35	6510 ± 560	6330 ± 1360
	1c	86 ± 6	93 ± 4	5680 ± 1000	7870 ± 160
	1d	74 ± 11	442 ± 36	7680 ± 1410	50700 ± 2160
	1e	111 ± 3	198 ± 44	7520 ± 710	14260 ± 590
S166C	1a	10 ± 1	20 ± 1	1160 ± 140	4920 ± 1320
	1c	17 ± 1	68 ± 2	1746 ± 120	5798 ± 106
	1d	16 ± 1	72 ± 3	2370 ± 91	11460 ± 400
	1e	14 ± 0	67 ± 3	784 ± 75	5198 ± 145

^a Mean ± standard error from 4 replicates, obtained at room temperature (see text).

^b Values and error calculated from individual k_{cat} and K_M values obtained at 25°C.

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The factor by which amidase k_{cat}/K_M values for N62C-**a** and S166C-**a** differed from WT was the same for the screen and the characterized CMMs, indicating that the screen was giving the correct relative pattern for amidase activity. With respect to esterase, the k_{cat}/K_M values for WT and N62C-**a** were the same in the screen and the characterized enzyme (Table 3), consistent with validation results. For S166C-**a**, however, the screen underestimated the esterase k_{cat}/K_M value ~5-fold. Given that the amidase value for S166C-**a** was not underestimated, the reason for the discrepancy could not be significant denaturation. The seven WT control treatments had the same esterase and amidase activity (and hence esterase/amidase ratio, Figure 3), indicating that the reagents themselves did not cause differential denaturation.

The screen results (Figure 4) suggested that N62C-**d** and **e** had greatly improved esterase activity as compared to WT. In the 166 family, some CMMs appeared to have very favourable esterase/amidase ratios. Members of the 217 family were intermediate with respect to esterase and esterase/amidase ratio. To determine the reliability of these results, N62C- and S166C-**c**, **d**, and **e** were prepared and characterized. The k_{cat}/K_M values from the screen and the characterized enzymes agreed within limits of error discussed above, except for both 4-carboxybenzyl (**d**) CMMs for which amidase and esterase were both ~5-

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